CLAIMS

1. Decarbamylase crystal having a space group $P2_12_12$ in the orthorhombic system and an amino acid sequence set forth in SEQ ID NO.: 1, or a space group $P2_12_12_1$ in the orthorhombic system and an amino acid sequence set forth in SEQ ID NO.: 2.

2. Decarbamylase crystal according to claim 1, wherein the crystal has a unit cell in the form of a rectangular parallelepiped and has lattice constants: a=66.5-68.5 Å, b=135.5-138.0 Å, and c=66.5-68.5 Å; and the amino acid sequence is SEQ ID NO.: 1.

3. Decarbamylase crystal according to claim 1, wherein the crystal has a unit cell in the form of a rectangular parallelepiped and has lattice constants: a=68.5-70.5 Å, b=138.0-140.5 Å, and c=68.5-73.0 Å; and the amino acid sequence is SEQ ID NO.: 1.

4. Decarbamylase crystal according to claim 1, wherein the crystal has a unit cell in the form of a rectangular parallelepiped and has lattice constants: a=81.5-82.5 Å, b=133.0-135.0 Å, and c=119.5-121.5 Å; and the amino acid sequence is SEQ ID NO.: 2.

5. Crystal according to any one of claims 1-4, wherein the crystal contains at least one or more heavy metal atoms per decarbamylase molecule.

6. Crystal according to claim 5, wherein the heavy metal atom is any of mercury, gold, platinum, lead, iridium, osmium, and uranium.

7. Frozen crystal, prepared by freezing decarbamylase crystal according to any one of claims 1-6 in liquid nitrogen.

8. A method for preparing a crystal of decarbamylase, comprising the steps of: providing decarbamylase solution having a concentration of 1-50 mg/ml; providing precipitant solution containing polyethylene glycol (PEG) or methoxypolyethylene glycol (PEGMME) having a concentration of 5-30 wt%, and a buffer agent having a concentration such that pH 6.0-9.0 is provided; mixing the decarbamylase solution with the precipitant solution; and allowing the resultant mixture solution to stand for a predetermined period of time until the decarbamylase crystal is grown in the solution to a predetermined size or more.

9. A method according to claim 8, wherein the mixing step comprises mixing a droplet of the decarbamylase solution with a droplet of the precipitant solution, and the step of allowing the resultant mixture solution to stand comprises suspending the mixture droplet obtained in the mixing step on a solution reservoir holding the precipitant solution in a sealed container, wherein the precipitant solution in the solution reservoir has a vapor pressure lower than a vapor pressure of the mixture droplet.

10. A method according to claim 8, wherein the mixing step comprises mixing a droplet of the decarbamylase solution with a droplet of the precipitant solution, and the step of allowing the resultant mixture solution to stand comprises suspending the mixture droplet obtained in the mixing step on a droplet stage of a solution reservoir holding the precipitant solution in a sealed container, wherein the precipitant solution in the solution reservoir has a vapor

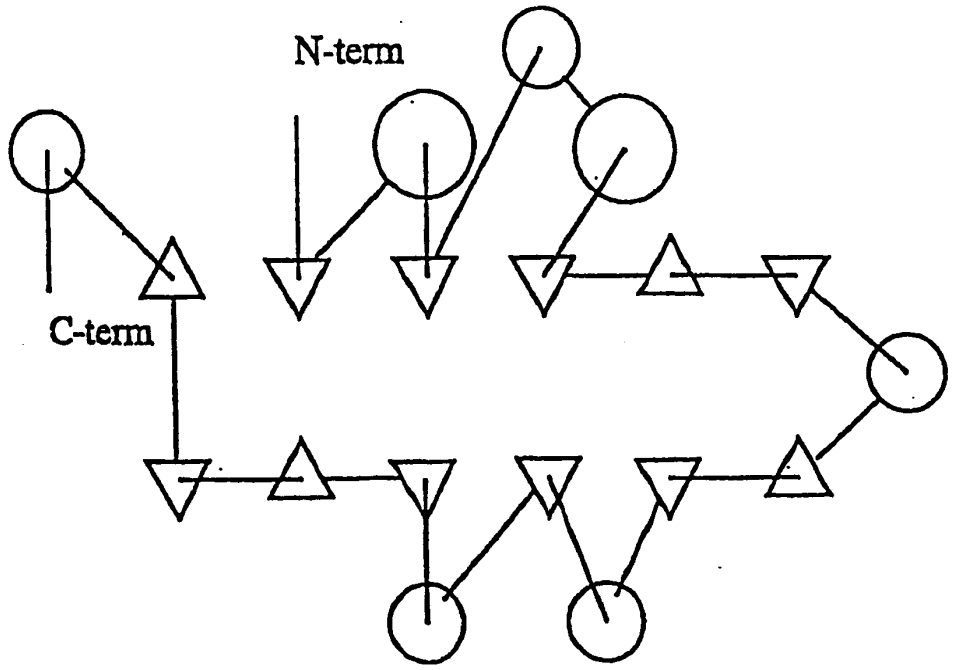
pressure lower than a vapor pressure of the mixture droplet.

11. A method according to claim 8, wherein the predetermined period of time during which the mixture solution is allowed to stand is one day to three weeks.

12. A method according to claim 8, further comprising placing the decarbamylase solution in a size exclusion semi-permeable membrane after the step of providing the decarbamylase solution, wherein the mixing step comprises diffusing the precipitant solution through the semi-permeable membrane into the decarbamylase solution.

13. A method according to claim 8, wherein the mixing step comprises gradually adding the precipitant solution to the decarbamylase solution, and the step of allowing the resultant mixture solution to stand comprises allowing the mixture solution to stand in a sealed container.

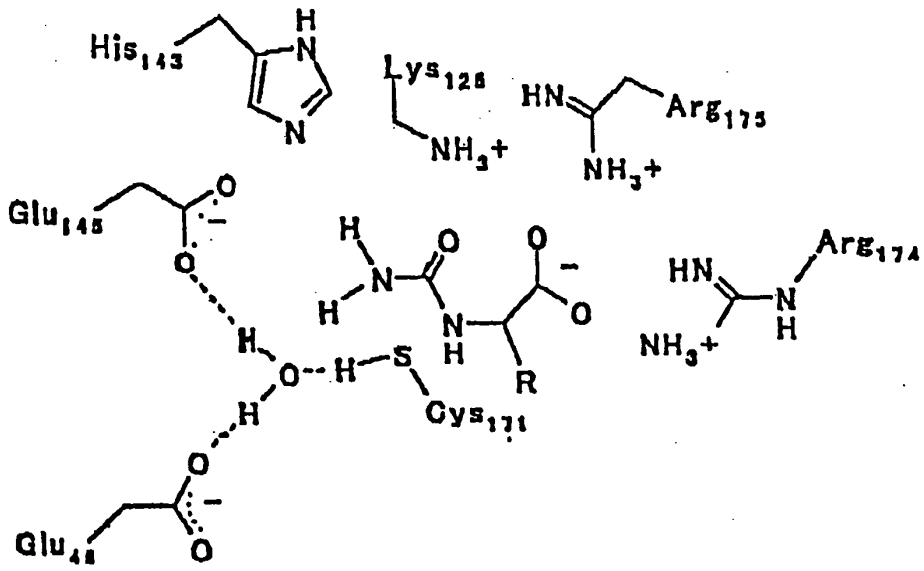
14. Decarbamylase characterized by a stereostructure having protein stereostructure topology represented in the following figure:



or an active fragment thereof.

15. Decarbamylase having a four-layer sandwich structure containing a secondary structure containing four α helices and twelve β sheets, or an active fragment thereof.

16. Decarbamylase, wherein amino acid residues thereof involved in an enzyme reaction are one cysteine residue, two glutamic acid residues; one lysine residue, and a substrate of the enzyme reaction is D-N-carbamoyl-α-amino acid; and a substrate-binding active site thereof is characterized by a stereostructure represented by:



where a substitute R is a side chain of D-N-carbamoyl-α-amino acid, or a decarbamylase mutant, or an active fragment thereof.

17. An enzyme molecule having decarbamylase activity wherein a substrate thereof is D-N-carbamoyl-α-amino acid, wherein the enzyme molecule has an active site cavity formed of at least amino acids corresponding to the following amino acids of SEQ ID NO.: 1 or 2: Glu at position 46, Lys at position 126, Glu at position 145, and Cys at position 171, or an active fragment thereof.

18. An enzyme according to claim 17, wherein in a reaction,

the D-N-carbamoyl-α-amino acid can interact with amino acids corresponding to Lys at position 126, His at position 143, Glu at position 145, Arg at position 174, Arg at position 175, and Thr at position 197 of SEQ ID NO.: 1 or 2 at the active site cavity, or an active fragment thereof.

19. An enzyme according to claim 17 or 18, wherein amino acids corresponding to Glu at position 46, Glu at position 145, and Cys at position 171 of SEQ ID NO.: 1 or 2 have a hydrogen bond via a water molecule at the active site cavity, or an active fragment thereof.

20. An enzyme molecule according to any one of claims 16-19, wherein the D-N-carbamoyl-α-amino acid is selected from the group consisting of D-N-carbamoyl-phenylglycine, D-N-carbamoyl-parahydroxyphenylglycine, D-N-carbamoyl-phenylalanine, D-N-carbamoyl-valine, D-N-carbamoyl-alanine, D-N-carbamoyl-cysteine, D-N-carbamoyl-aspartic acid, D-N-carbamoyl-glutamic acid, D-N-carbamoyl-glycine, D-N-carbamoyl-histidine, D-N-carbamoyl-isoleucine, D-N-carbamoyl-lysine, D-N-carbamoyl-leucine, D-N-carbamoyl-methionine, D-N-carbamoyl-asparagine, D-N-carbamoyl-proline, D-N-carbamoyl-glutamine, D-N-carbamoyl-arginine, D-N-carbamoyl-serine, D-N-carbamoyl-threonine, D-N-carbamoyl-tryptophan, and D-N-carbamoyl-tyrosine, or an active fragment thereof.

21. A decarbamylase complex characterized by a stereostructure of a complex of decarbamylase, a mutant thereof, or an active fragment thereof, and D-N-carbamoyl-α-amino acid or D-α-amino acid, wherein the complex is constructed with a molecular design technique

from a stereostructure of decarbamylase according to claim 14 or 15.

22. A method for designing decarbamylase mutants, comprising the step of designing the decarbamylase mutants having a physical property and/or a function modified based on a stereostructure of decarbamylase according to any one of claims 14, 16, and 21.

23. A method for designing decarbamylase mutants, comprising the step of: preparing a crystal of an enzyme having decarbamylase activity; determining a stereostructure of the crystal by subjecting the crystal to X-ray crystallography; and designing the decarbamylase mutants having an improved physical property and/or function based on the determined stereostructure.

24. A method according to claim 23, wherein the stereostructure is a stereostructure of decarbamylase according to any one of claims 14, 16, and 21.

25. A method for designing decarbamylase mutants, comprising the step of: preparing a crystal of an enzyme having decarbamylase activity; determining a stereostructure of the crystal by subjecting the crystal to X-ray crystallography; designing the decarbamylase mutants having an improved physical property and/or function based on the determined stereostructure; and producing the decarbamylase mutants.

26. A method according to claim 25, wherein the stereostructure is a stereostructure of decarbamylase according to any one of claims 14, 16, and 21.

27. A method according to claim 26, wherein the step of designing the decarbamylase mutants is intended for a modification of one or more characteristics of the enzyme selected from the group consisting of a change in substrate specificity, a change in specific activity, an improvement in stability, optimization of optimum pH, and a change in water solubility.

28. A method according to claim 27, wherein the modification of the characteristics of the enzyme includes an improvement in stability.

29. A method according to claim 28, wherein the mutant designing for an improvement in stability includes a mutation including substitution of an amino acid residue which leads to a reduction in activity due to air oxidation.

30. A method according to claims 27, wherein the modification of the characteristics of the enzyme includes a change in specific activity and optimization of optimum pH.

31. A decarbamylase mutant obtained with a production method according to any one of claims 25-30.

32. A method for modifying a polypeptide or protein enzyme having a primary amino acid sequence similar to that of decarbamylase by utilizing a stereostructure of decarbamylase crystal according to any one of claims 1-7, or a stereostructure of decarbamylase according to any one of claims 14, 16, and 21.

33. A system for designing decarbamylase mutants using a

computer, comprising:

means for determining a stereostructure of crystal of an enzyme having decarbamylase activity; and

means for designing the decarbamylase mutants having a physical property and/or a function improved based on the determined stereostructure.

34. A computer readable recording medium recording a program for executing a process for designing decarbamylase mutants, wherein the designing process comprises the steps of:

inputting data of crystal of an enzyme having decarbamylase activity determined by subjecting the crystal to X-ray crystallography; and

designing the decarbamylase mutants having a physical property and/or a function improved based on the determined stereostructure.

35. A recording medium recording data describing a stereostructure of a decarbamylase mutant obtained by a process comprising the steps of:

inputting data of crystal of an enzyme having decarbamylase activity determined by subjecting the crystal to X-ray crystallography; and

designing the decarbamylase mutant having a physical property and/or a function improved based on the determined stereostructure.